

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: CHEN, ZHIJIAN J.
- (ii) TITLE OF INVENTION: A KINASE CAPABLE OF SITE-SPECIFIC PHOSPHORYLATION OF I κ B α
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: US
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/825,559
 - (B) FILING DATE: 19-MAR-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/616,499
 - (B) FILING DATE: 19-MAR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BROWN, ANNE
 - (B) REGISTRATION NUMBER: 36,463
 - (C) REFERENCE/DOCKET NUMBER: 1448.0240001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 371-2600
 - (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGTGACCTC AGGATATCGA GAGCAATACT TCCATT

(2) INFORMATION FOR SEQ ID NO:2:

(ii) MOLECULE TYPE: cDNA

TTGTGACCTC AGGATATCGA GAGAAATACT TCCAT

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 1
      (D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"
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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 5
      (D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"
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Xaa Tyr Val Glu Xaa Glu Arg
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

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(ix) FEATURE:
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      (B) LOCATION: 1
      (D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"
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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 2
      (D) OTHER INFORMATION: /note= "CAN BE GLN OR LYS"
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(A) NAME/KEY: Modified-site
(B) LOCATION: 5
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(A) NAME/KEY: Modified-site
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(A) NAME/KEY: Modified-site
(B) LOCATION: 9
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"

Xaa Xaa Glu Val Xaa Glu Thr Xaa Xaa Ser Xaa Glu Lys
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 1
      (D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"
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(ix) FEATURE:
      (A) NAME/KEY: Modified-site
      (B) LOCATION: 7
      (D) OTHER INFORMATION: /note= "CAN BE LEU OR ILE"
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Xaa Phe Thr Thr Met Glu Xaa Met Arg
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Tyr His Ala Leu Ser Asn Leu Pro Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGGTGACGAG TGGTGGCCGA AGCAGGGGGA CAGCAAGGGA CGCTCAGGCG GGGACCATGG	60
CGGACGGCGG CTCGGAGCGG GCTGACGGGC GCATCGTCAA GATGGAGGTG GACTACAGCG	120
CCACGGTGGA TCAGCGCCTA CCCGAGTGTG CGAAGTATGC CAAGGAAGGA AGACTTCAAG	180
AAGTCATTGA AACCCTTCTC TCTCTGAAA AGCAGACTCG TACTGCTTCC GATATGGTAT	240
CGACATCCCG TATCTTAGTT GCAGTAGTGA AGNTGTGCTA TGAGGCTAAA GAATGGGATT	300
TACTTAATTA AAAATATTAT TGCTTTTTGT CCAAAGGCG GAGTCAAGTT AAAACAAGC	360
TAGTTGACAA AAAATGGATT NAACAGTTGC TGTNACTTAT TGTT	404

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATACCAAGAG GTACCAGGAA GCATTGCATT TGGGTTCTCA GCTGCTGCGG GAGTTGAAAA	60
AGATGGACGA CAAAGCTCTT TTGGTGGAAG TACAGCTTTT AGAAAGCAAA ACATACCATG	120
CCCTGAGCAA CCTGCCGAAA GCCCAGCTG CCTTAACTTC TTCTCGAACC ACAGCAAATG	180
CCATCTACTG CCCCTAAAT TGCAGGCCAC CTTGGACATG CAGTCGGGTA TTATCCATGC	240
AGCAGAAGAG AAGGCTTGAA ACTCGTACTC ATACTTCTAT GAGGCATTTA GGGTATGACT	300
CATCGACAGC CCAAGGCATC ACA	323